

SCORE Search Results Details for Application 10552515 and Search Result 20080630_144100_us-10-552-515-7.rpr.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080630_144100_us-10-552-515-7.rpr.

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OM protein - protein search, using sw model

Run on: June 30, 2008, 17:45:41 ; Search time 6 Seconds
(without alignments)
157.446 Million cell updates/sec

Title: US-10-552-515-7
Perfect score: 40
Sequence: 1 ILILSKIYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	33	82.5	521	2	A99100	phosphatidylinosit
2	32	80.0	98	2	T47314	hypothetical prote

3	32	80.0	117	2	H86640	ribonuclease P (EC
4	32	80.0	148	2	H72781	hypothetical prote
5	32	80.0	735	2	T39464	hypothetical prote
6	31	77.5	264	2	T26558	hypothetical prote
7	31	77.5	285	2	T01119	hypothetical prote
8	31	77.5	314	2	T11711	probable small GTP
9	31	77.5	758	2	S46625	finger protein YJL
10	30	75.0	143	2	F95116	GtrA family protei
11	30	75.0	143	2	D97986	mesH proteins [imp
12	30	75.0	204	2	S22616	hypothetical prote
13	30	75.0	260	2	G64690	type IIS restricti
14	30	75.0	286	2	G90140	conserved hypothet
15	30	75.0	306	2	B82396	probable chemotaxi
16	30	75.0	365	2	T04718	hypothetical prote
17	30	75.0	486	2	T44639	capsular polysacch
18	30	75.0	848	2	H64208	oligopeptide trans
19	30	75.0	861	2	S59770	probable membrane
20	30	75.0	1022	2	S50534	hypothetical prote
21	30	75.0	1223	2	S43579	C28A5.1 protein (c
22	29	72.5	127	2	S02163	spore germination
23	29	72.5	156	2	D81343	probable integral
24	29	72.5	166	2	F97128	probable membrane
25	29	72.5	191	2	D86358	hypothetical prote
26	29	72.5	249	2	C83795	hypothetical prote
27	29	72.5	255	1	SNHUC8	proteasome endopep
28	29	72.5	255	1	SNRTC8	proteasome endopep
29	29	72.5	255	2	S38529	proteasome endopep
30	29	72.5	280	2	C82490	probable potassium
31	29	72.5	325	2	JN0148	necdin, brain - mo
32	29	72.5	329	2	JC5173	stress response pr
33	29	72.5	330	2	T29675	hypothetical prote
34	29	72.5	346	2	E72672	hypothetical prote
35	29	72.5	359	2	B59105	hypothetical prote
36	29	72.5	381	2	G89009	protein R08F11.5 [
37	29	72.5	393	2	H72352	lipopolysaccharide
38	29	72.5	411	2	A96985	uncharacterized co
39	29	72.5	443	2	B26696	hypothetical prote
40	29	72.5	445	2	E22845	hypothetical prote
41	29	72.5	450	2	T25542	hypothetical prote
42	29	72.5	564	2	G86358	protein Similar to
43	29	72.5	595	2	AI0042	thiol, disulfide in
44	29	72.5	617	2	D90487	maltose ABC transp
45	29	72.5	746	2	S67203	probable membrane

ALIGNMENTS

RESULT 1

A99100

phosphatidylinositol 4-kinase [imported] - Guillardia theta nucleomorph

C;Species: nucleomorph Guillardia theta

A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: A99100

R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reith, M.; Cavalier-Smith, T.; Maier, U.G.

Nature 410, 1091-1096, 2001

A;Title: The highly reduced genome of an enslaved algal nucleus.

A;Reference number: A99082; MUID:11323671; PMID:11323671

A;Accession: A99100

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-521 <DOU>

A;Cross-references: UNIPROT:Q98RM0; UNIPARC:UPI000009662D; GB:AF165818; NID:g13794553; PIDN:

AAK39928.1; GSPDB:GN00150

C;Genetics:

A;Gene: PI4K

A;Map position: 1

A;Genome: nucleomorph

C;Keywords: nucleomorph

Query Match 82.5%; Score 33; DB 2; Length 521;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
 | :|||||:
 Db 234 IFLLSKIYI 242

RESULT 2

T47314

hypothetical protein T12K4.10 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T47314

R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer,

K.F.X.; Quetier, F.; Salanoubat M.Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A;Reference number: Z24460

A;Accession: T47314

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <MON>

A;Cross-references: UNIPROT:Q9M2A8; UNIPARC:UPI00000A9E99; EMBL:AL138640

A;Experimental source: cultivar Columbia; BAC clone T12K4

C;Genetics:

A;Map position: 3

A;Introns: 50/3; 74/3

A;Note: T12K4.10

Query Match 80.0%; Score 32; DB 2; Length 98;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
 | :|| |:
 Db 33 IILKKLYV 41

RESULT 3

H86640

ribonuclease P (EC 3.1.26.5) [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: *Lactococcus lactis* subsp. *lactis*
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
 C;Accession: H86640
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, S.D.; Sorokin, A.
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. *lactis* IL1403.
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: H86640
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-117 <STO>
 A;Cross-references: UNIPROT:Q9CJ73; UNIPARC:UPI000013442D; GB:AE005176; PID:g12722976; PIDN:AAK04226.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: rnpA
 C;Superfamily: bacterial ribonuclease P, protein component
 C;Keywords: hydrolase

Query Match 80.0%; Score 32; DB 2; Length 117;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
 :| |||||
 Db 104 VLKLSKIYV 112

RESULT 4
 H72781
 hypothetical protein APE0241 - *Aeropyrum pernix* (strain K1)
 C;Species: *Aeropyrum pernix*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: H72781
 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba, S.; Ankai, A.; Kosugi, H.; Hosoyama, A.; Fukui, S.; Nagai, Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura, Y.; Nomura, N.; Sako, Y.; Kikuchi, H.
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum pernix* K1.
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: H72781
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-148 <KAW>
 A;Cross-references: UNIPROT:Q9YFK7; UNIPARC:UPI000005DA72; DDBJ:AP000058; NID:g5103388; PIDN:BAA79154.1; PID:d1042930; PID:g5103633
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE0241
 C;Superfamily: *Aeropyrum pernix* hypothetical protein APE0241

Query Match 80.0%; Score 32; DB 2; Length 148;

Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
|::|||:|:
Db 89 IVLLSKLYI 97

RESULT 5

T39464

hypothetical protein SPBC1539.05 - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T39464

R;Mc Dougall, R.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Quail, M.; Harris, D.
submitted to the EMBL Data Library, July 1999

A;Reference number: Z21856

A;Accession: T39464

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-735 <MCD>

A;Cross-references: UNIPROT:Q9Y7Z4; UNIPARC:UPI000006BCF4; EMBL:AL096874; PIDN:CAB51337.1;

GSPDB:GN00067; SPDB:SPBC1539.05

A;Experimental source: strain 972h-; cosmid c1539

C;Genetics:

A;Gene: SPDB:SPBC1539.05

A;Map position: 2

A;Introns: 23/3; 157/3; 214/3; 260/3; 337/3; 516/3

Query Match 80.0%; Score 32; DB 2; Length 735;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILILSKIY 8
::|||||
Db 505 LIILSKIY 512

RESULT 6

T26558

hypothetical protein Y24F12A.a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26558

R;Lennard, N.

submitted to the EMBL Data Library, September 1999

A;Reference number: Z20233

A;Accession: T26558

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-264 <WIL>

A;Cross-references: UNIPROT:Q9TVH6; UNIPARC:UPI000017BC4F; EMBL:AL110480; NID:e1542182;

PIDN:CAB54377.1; CESP:Y24F12A.a

A;Experimental source: clone Y24F12A

C;Genetics:

A;Gene: CESP:Y24F12A.a

A;Introns: 36/2; 68/1; 216/3

Query Match 77.5%; Score 31; DB 2; Length 264;
 Best Local Similarity 85.7%; Pred. No. 46;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILSKIYV 9
 |||||:
 Db 228 ILSKIYI 234

RESULT 7

T01119
 hypothetical protein At2g32880 [imported] - Arabidopsis thaliana
 N;Alternate names: hypothetical protein T21L14.18
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C;Accession: T01119; F84738
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
 submitted to the EMBL Data Library, December 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence.
 A;Reference number: Z14209
 A;Accession: T01119
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-285 <ROU>
 A;Cross-references: UNIPROT:O48777; UNIPARC:UPI000009E1EC; EMBL:AC003033; NID:g2702261; PID:g2702282
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H. M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: F84738
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-285 <STO>
 A;Cross-references: UNIPARC:UPI000009E1EC; GB:AE002093; NID:g2702282; PIDN:AAB91985.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: T21L14.18; At2g32880
 A;Map position: 2
 A;Introns: 11/1; 54/2; 105/1; 206/2
 C;Superfamily: Arabidopsis thaliana hypothetical protein A_TM018A10.12

Query Match 77.5%; Score 31; DB 2; Length 285;
 Best Local Similarity 55.6%; Pred. No. 50;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
 ||: ||:|:
 Db 269 ILLFSKLYI 277

RESULT 8

T11711
 probable small GTPase - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T11711
 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1998
 A;Reference number: Z17318
 A;Accession: T11711
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-314 <SEE>
 A;Cross-references: UNIPROT:O74544; UNIPARC:UPI000006C651; EMBL:AL031532; NID:e1319424; PID:e1319429
 A;Experimental source: strain 972h(-)
 C;Genetics:
 A;Map position: IIIR
 A;Introns: 47/2
 A;Note: SPCC777.05

Query Match 77.5%; Score 31; DB 2; Length 314;
 Best Local Similarity 85.7%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILSKIYV 9
 :|||||
 Db 204 VLSKIYV 210

RESULT 9

S46625
 finger protein YJL206c - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: probable membrane protein YJL206c; protein J0316
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
 C;Accession: S46625; S56993
 R;Purnelle, B.; Coster, F.; Goffeau, A.
 Yeast 10, 1235-1249, 1994
 A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1 and two homologues to chromosome III genes.
 A;Reference number: S46621; MUID:95274326; PMID:7754713
 A;Accession: S46625
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-758 <PUR>
 A;Cross-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:g1183992; PIDN:CAA54752.1; PID:g547586
 R;Purnelle, B.; Coster, F.; Goffeau, A.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56977
 A;Accession: S56993
 A;Molecule type: DNA
 A;Residues: 1-758 <PUW>

A;Cross-references: UNIPARC:UPI000013B60A; EMBL:Z49481; NID:g1015584; PIDN:CAA89502.1; PID:g1015585; MIPS:YJL206c
 C;Genetics:
 A;Cross-references: SGD:S0003741
 A;Map position: 10L
 C;Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc finger
 F;42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 77.5%; Score 31; DB 2; Length 758;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILILSKIY 8
 |||:|:|
 Db 409 ILIMSRIY 416

RESULT 10

F95116
 GtrA family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: F95116
 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J. F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D. A.; Hollingshead, S.K.; Fraser, C.M.
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: F95116
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-143 <KUR>
 A;Cross-references: UNIPROT:Q97R28; UNIPARC:UPI000005169E; GB:AE005672; PIDN:AAK75127.1; PID:g14972484; GSPDB:GN00164; TIGR:SP4SP1011
 A;Experimental source: strain TIGR4
 C;Genetics:
 A;Gene: SP1011

Query Match 75.0%; Score 30; DB 2; Length 143;
 Best Local Similarity 71.4%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILSKIYV 9
 ||||:|:
 Db 134 ILSKVYI 140

RESULT 11

D97986
 mesH proteine [imported] - Streptococcus pneumoniae (strain R6)
 C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C;Accession: D97986
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
 Estrem, S.; Fritz, L.; Fu, D.J.; Fuller, W.; Geringer, C.; Gilmour, R.; Glass, J.S.; Khoja,
 H.; Kraft, A.; LaGace, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima,
 P.; McAhren, S.; McHenney, M.; McLeaster, K.; Mundy, C.; Nicas, T.I.; Norris, F.H.; O'Gara,
 M.; Peery, R.; Robertson, G.T.; Rockey, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 Rostek Jr., P.R.; Skatrud, P.L.; Glass, J.I.
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234
 A;Accession: D97986
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-143 <KUR>
 A;Cross-references: UNIPROT:Q8DQ02; UNIPARC:UPI00000E3559; GB:AE007317; PIDN:AAK99720.1;
 PID:g15458524; GSPDB:GN00174
 C;Genetics:
 A;Gene: mesh

Query Match 75.0%; Score 30; DB 2; Length 143;
 Best Local Similarity 71.4%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILSKIYV 9
 |||||:
 Db 134 ILSKVYI 140

RESULT 12
 S22616
 hypothetical protein 14.9 - Salmonella choleraesuis
 C;Species: Salmonella choleraesuis
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 22-Oct-1999
 C;Accession: S22616
 R;Brown, P.K.; Romana, L.K.; Reeves, P.R.
 Mol. Microbiol. 6, 1385-1394, 1992
 A;Title: Molecular analysis of the rfb gene cluster of Salmonella serovar muenchen (strain
 M67): the genetic basis of the polymorphism between groups C2 and B.
 A;Reference number: S22613; MUID:92349966; PMID:1379320
 A;Accession: S22616
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-204 <BRO>
 A;Cross-references: UNIPARC:UPI00000BBBEC; EMBL:X61917; NID:g47004; PIDN:CAA43910.1; PID:
 g47008
 C;Superfamily: galactoside acetyltransferase

Query Match 75.0%; Score 30; DB 2; Length 204;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
 ||| |||:
 Db 113 ILIGSKVYI 121

RESULT 13

G64690

type IIS restriction enzyme M1 protein - *Helicobacter pylori* (strain 26695)

C;Species: *Helicobacter pylori*

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: G64690

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D. E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J. M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: G64690

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-260 <TOM>

A;Cross-references: UNIPROT:O25920; UNIPARC:UPI00000D30C7; GB:AE000637; GB:AE000511; NID: g2314536; PIDN:AAD08411.1; PID:g2314538; TIGR:HP1367

C;Genetics:

A;Start codon: TTG

C;Superfamily: type II site-specific DNA-methyltransferase

Query Match	75.0%	Score 30;	DB 2;	Length 260;
Best Local Similarity	62.5%	Pred. No. 76;		
Matches	5;	Conservative	3;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy 2 LILSKIYV 9

:||:||||:

Db 1 MILNKIYI 8

RESULT 14

G90140

conserved hypothetical protein [imported] - *Sulfolobus solfataricus*

C;Species: *Sulfolobus solfataricus*

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: G90140

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Weiher, C.C.Y.; Clausen, I.G.; Curtis, B.A.; De Moors, A.; Erauso, G.; Fletcher, C.; Gordon, P.M.K.; Heikamp-de Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; Schenk, M.E.; Theriault, C.; Tolstrup, N.; Charlebois, R.L.; Doolittle, W.F.; Duguet, M.; Gaasterland, T.; Garrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: *Sulfolobus solfataricus* complete genome.

A;Reference number: A99139

A;Accession: G90140

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-286 <KUR>

A;Cross-references: UNIPROT:Q981D0; UNIPARC:UPI0000064167; GB:AE0006641; NID:g13813144; PIDN:

AAK40382.1; GSPDB:GN00155

C;Genetics:

A;Gene: SS00015

Query Match 75.0%; Score 30; DB 2; Length 286;
 Best Local Similarity 55.6%; Pred. No. 83;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILILSKIYV 9
 |::||::||
 Db 114 IVLLSQVYV 122

RESULT 15

B82396

probable chemotaxis protein CheV VCA0954 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: B82396

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T. D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: B82396

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-306 <HEI>

A;Cross-references: UNIPROT:Q9KKZ6; UNIPARC:UPI00000C36E3; GB:AE004422; GB:AE003853; NID: g9658387; PIDN:AAF96850.1; GSPDB:GN00127; TIGR:VCA0954

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0954

A;Map position: 2

Query Match 75.0%; Score 30; DB 2; Length 306;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LILSKIY 8
 |:|||||
 Db 146 LLLSKIY 152

Search completed: June 30, 2008, 17:46:48

Job time : 8.375 secs

SCORE 3.6